530 326

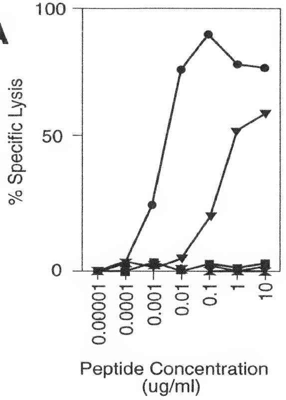
08/417,174

5844075

FIG. 1

```
   1  AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA    59
                                                            MetPro     2

  60  AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC  119
   3  ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr   22

 120  ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC  179
  23  ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu   42

 180  ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT  239
  43  IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu   62

 240  CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG  299
  63  HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg   82

 300  GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT  359
  83  AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro  102

 360  GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG  419
 103  AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro

 420  AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC  479

 480  ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC  539
 540  AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA  599
 600  TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA  659
 660  GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT  719
 720  GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG  779
 780  AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG  839
 840  GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT  899
 900  CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC  959
 960  CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG 1019
1020  GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG 1079
1080  CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT 1139
1140  AGTAGAGACGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA 1199
1200  TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT 1259
1260  GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC 1319
1320  AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT 1379
1380  AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG 1439
1440  TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG 1499
1500  AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1559
```

FIG. 2A


100
50
0
% Specific Lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide Concentration
(ug/ml)

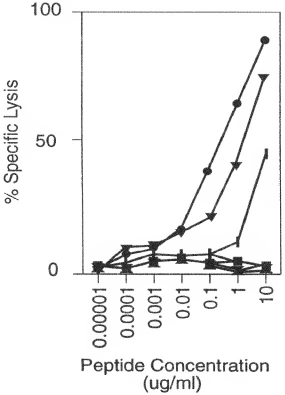

100
50
0
% Specific Lysis
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide Concentration
(ug/ml)

FIG. 2B

FIG. 3A

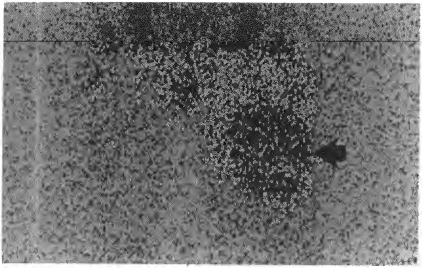
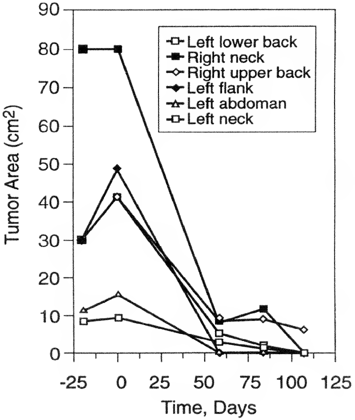


FIG. 3B



Left lower back
Right neck
Right upper back
Left flank
Left abdoman
Left neck
Tumor Area (cm^2)
Time, Days
90
80
70
60
50
40
30
20
10
0
-25
0
25
50
75
100
125

FIG. 4A

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280
TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720
GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920
GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIG. 4B

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA 1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA 1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC 1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG 1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC 1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC 2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT 2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160
AAAAAAAAAA AA 2172

FIG. 5A

1	MDLVLKRCLL	HLAVIGALLA	VGATKVPRNQ	DWLGVSRQLR	TKAWNRQLYP
51	EWTEAQRLDC	WRGGQVSLKV	SNDGPTLIGA	NASFSIALNF	PGSQKVLPDG
101	QVIWVNNTII	NGSQVWGGQP	VYPQETDDAC	IFPDGGPCPS	GSWSQKRSFV
151	YVWKTWGQYW	QFLGGPVSGL	SIGTGRAMLG	THTMEVTVYH	RRGSRSYVPL
201	AHSSSAFTIT	DQVPFSVSVS	QLRALDGGNK	HFLRNQPLTF	ALQLHDPSGY
251	LAEADLSYTW	DFGDSSGTLI	SRALVVTHTY	LEPGPVTAQV	VLQAAIPLTS
301	CGSSPVPGTT	DGHRPTAEAP	NTTAGQVPTT	EVVGTTPGQA	PTAEPSGTTS
351	VQVPTTEVIS	TAPVQMPTAE	STGMTPEKVP	VSEVMGTTLA	EMSTPEATGM
401	TPAEVSIVVL	SGTTAAQVTT	TEWVETTARE	LPIPEPEGPD	ASSIMSTESI
451	TGSLGPLLDG	TATLRLVKRQ	VPLDCVLYRY	GSFSVTLDIV	QGIESAEILQ
501	AVPSGEGDAF	ELTVSCQGGL	PKEACMEISS	PGCQPPAQRL	CQPVLPSPAC
551	QLVLHQILKG	GSGTYCLNVS	LADTNSLAVV	STQLIMPGQE	AGLGQVPLIV
601	GILLVLMAVV	LASLIYRRRL	MKQDFSVPQL	PHSSSHWLRL	PRIFCSCPIG
651	ENSPLLSGQQ	V			

FIG. 5B

```
Pmel17     M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20       M-----V-----Q-----L-----......------------
gp100      M-----V-----Q-----L-----......------------
cDNA25FL   M-----F-----Q-----L-----......------------
cDNA25TR               Q-----L-----......-----PPQWAAGLSTLI
           1    162   236   274   588        649
```

FIG. 6A

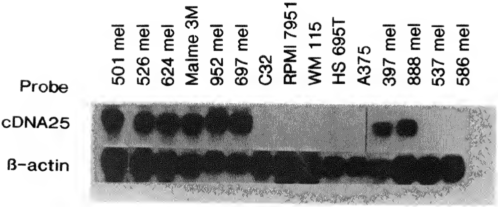


FIG. 6B

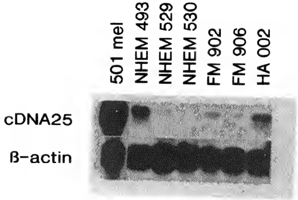


FIG. 6C

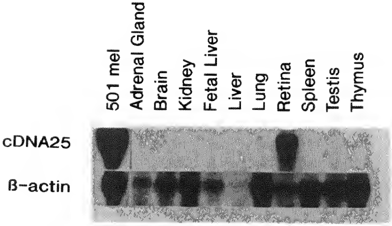


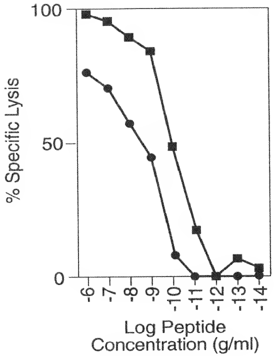
FIG. 7A

```
 1       MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
        D3---------- ---------- ---------- ---------- ----------
        D5---------- ---------- ---------- ---------- ----------
        D4---------- ---------- ---------- ---------- ----------
        C4---------- ---------- ---------- ---------- ----------
 51      EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
        D3---------- ---------- ---------- ---------- ----------
        D5---------- ---------- ---------- ---------- ----------
        D4---------- ---------- ---------- ---------- ----------
        C4---------- ---------- ---------- ---------- ----------
101      QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
        D3---------- ---------- ---------- ---------- ----------
        D5---------- ---------- ---------- ---------- ----------
        D4---------- ---------- ---------- ---------- ----------
        C4---------- ---------- ---------- ---------- ----------
151      YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
        D3----D3
        D5---------- ---D5
        D4---------- ---------- ---------- ---------- -----D4
        C4---------- ---------- ---------- ---------- ----------
201      AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
        C4---------- ---------- ---------- ---------- ----------
                                           25TR----- ----------
251      LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
        C4---------- ----------C4
      25TR---------- ---------- ---------- ---------- ----------
301      CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
      25TR---------- ---------- ---------- ---------- ----------
351      VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
      25TR---------- ---------- ---------- ---------- ----------
401      TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
      25TR---------- ---------- ---------- ---------- ----------
451      TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
      25TR---------- ---------- ---------- ---------- ----------
501      AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
      25TR---------- ---------- ---------- ---------- ----------
551      QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
      25TR---------- ---------- ---------- ---------- ----------
601      GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
      25TR---------- ---------- ---------- ---------- ----------
651      ENSPLLSGQQ V
         25TR---------- -25TR
```

FIG. 7B

DNA fragment	TIL 620-1	620-2	660-1	1143	1200
D3	−	−	−	−	−
D5	−	+	−	−	+
D4	−	+	−	−	+
C4	+	+	+	+	+
25TR	−	−	+	+	+

FIG. 8A


100
50
0
% Specific Lysis
-6
-7
-8
-9
-10
-11
-12
-13
-14
Log Peptide
Concentration (g/ml)

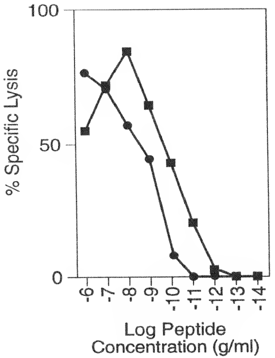
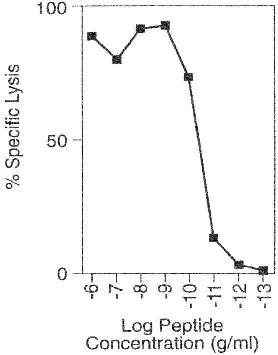

100
50
0
% Specific Lysis
-6
-7
-8
-9
-10
-11
-12
-13
-14
Log Peptide
Concentration (g/ml)

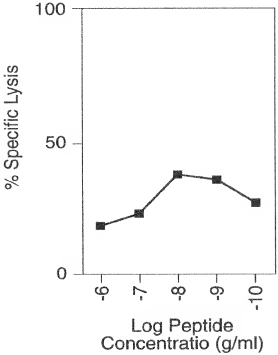
FIG. 8B

FIG. 8C



100
50
0
% Specific Lysis
-6
-7
-8
-9
-10
-11
-12
-13
Log Peptide
Concentration (g/ml)

FIG. 8D



100
50
0
% Specific Lysis
-6
-7
-8
-9
-10
Log Peptide
Concentratio (g/ml)